

WHAT IS CLAIMED IS:

1. A method for analyzing a nucleic acid sample
comprised of the steps:

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(a) forming labeled DNA sample fragments from a nucleic
acid sample;

10 (b) size separating said sample fragments with size
standard fragments, and detecting the fragments to form a sample
signal and a size standard signal;

(c) transforming the sample signal into size coordinates
using the size standard signal; and

(d) analyzing the nucleic acid sample in size
coordinates.

2. A method for analyzing a nucleic acid sample
comprised of the steps:

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(a) forming labeled DNA sample fragments from a nucleic
acid sample;

25 (b) size separating and detecting said sample fragments
to form a sample signal;

(c) forming labeled DNA ladder fragments corresponding
to molecular lengths;

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(d) size separating and detecting said ladder fragments
to form a ladder signal;

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(e) transforming the sample signal into length coordinates using the ladder signal; and

(f) analyzing the nucleic acid sample signal in length coordinates.

3. A method as described in Claim 2 wherein after the analyzing step (f) there is the additional step of determining a length or amount of a fragment in the nucleic acid sample.

4. A method as described in Claim 3 wherein after the determining step there is the additional step of finding a gene by positional cloning.

5. A method as described in Claim 3 wherein after the determining step there is the additional step of identifying an individual by DNA profiling.

6. A method for generating revenue from computer scoring of genetic data comprised of the steps:

(a) supplying a software program that automatically scores genetic data;

(b) forming genetic data that can be scored by the software program;

(c) scoring the genetic data using the software program to form a quantity of genetic data; and

(d) generating a revenue from computer scoring of genetic data that is related to the quantity.

7. A method as described in Claim 6 wherein prior to the step (d) of generating a revenue there are the steps of:

(e) defining a labor cost of scoring the quantity of genetic data when not using the software program;

(f) providing a calculating mechanism for estimating the labor cost from the quantity;

(g) determining the labor cost based on the quantity;
and

(h) establishing a price for using the software program that is related to the labor cost.

8. A method as described in Claim 7 wherein the calculating mechanism includes a spreadsheet.

9. A method as described in Claim 7 wherein the calculating mechanism is provided via the Internet.

10. A method as described in Claim 7 wherein the calculating mechanism operates interactively via the Internet.

11. A system for analyzing a nucleic acid sample comprising:

(a) means for forming labeled DNA sample fragments from a nucleic acid sample;

(b) means for size separating and detecting said sample fragments to form a sample signal, said separating and detecting means in communication with the sample fragments;

(c) means for forming labeled DNA ladder fragments corresponding to molecular lengths;

5 (d) means for size separating and detecting said ladder fragments to form a ladder signal, said separating and detecting means in communication with the ladder fragments;

10 (e) means for transforming the sample signal into length coordinates using the ladder signal, said transforming means in communication with the signals; and

(f) means for analyzing the nucleic acid sample signal in length coordinates, said analyzing means in communication with the transforming means.

15 12. A method for producing a nucleic acid analysis comprised of the steps:

20 (a) analyzing a first nucleic acid sample on a first size separation instrument to form a first signal;

(b) analyzing a second nucleic acid sample on a second size separation instrument to form a second signal;

25 (c) comparing the first signal with the second signal in a computing device with memory to form a comparison; and

30 (d) producing a nucleic acid analysis of the two samples from the comparison that is independent of the size separation instruments used.

13. A method as described in Claim 12 wherein the size separation instrument is a DNA sequencer that uses electrophoresis.

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14. A method as described in Claim 12 wherein the nucleic acid analysis characterizes a size or amount of DNA in one of the nucleic acid samples.

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15. A method as described in Claim 12 wherein the nucleic acid analysis finds a gene by positional cloning.

16. A method as described in Claim 12 wherein the nucleic acid analysis identifies an individual by DNA profiling.

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17. A method for resolving DNA mixtures comprised of the steps:

sample;

(a) obtaining DNA profile data that include a mixed

(b) representing the data in a linear equation;

(c) deriving a solution from the linear equation; and

(d) resolving the DNA mixture from the solution.

18. A method as described in Claim 17 wherein the obtaining step (a) includes the step of performing a PCR on an STR locus of an individual.

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19. A method as described in Claim 17 wherein the representing step (b) includes a matrix or vector representation.

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20. A method as described in Claim 17 wherein the deriving step (c) includes an optimization procedure.

21. A method as described in Claim 17 wherein the deriving step (c) includes a matrix operation.

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22. A method as described in Claim 17 wherein the 5 resolving step (d) produces the genotype of an individual.

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